

STIC-Biotech/ChemLib

129776

From: Winkler, Ulrike
Sent: Thursday, August 12, 2004 11:42 AM
To: STIC-Biotech/ChemLib

STIC

Please do a sequence alignment between the following sequences

SEQ ID NO: 1 of US Pat No. 5942607 and SEQ ID NO: 5 of application # 09/303510

and

SEQ ID NO: 2 of US Pat No. 5942607 and SEQ ID NO: 6 of application # 09/303510

CRFE

Thanks, Ulrike

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(103)

Freeman is human CD80
CD86

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Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

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LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
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IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 5942607-1_x_303510-5.res made by spaula on Tue 17 Aug 104 16:38:38-PST.

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Query sequence being compared: US-08-101-624-1 (1-1120)
Number of sequences searched: 1
Number of scores above cutoff: 1
```

```
720 730 740 750 760 770 780
TGTTCATTCCTGATGTTACGAGCAATATGACCATCTTCTGATTTCTGAACCT--GACA-AGACGCGC
|||||
TTTTCAGTCCCTGAAG-CAC--ACAATGTAGCGCTTTTGTGCCCT-GAACTGGAGACACTGGAGATGC
680 690 700 710 720 730 740
790 800 810 820 830 840 850
TTTTCATTCGACCTTCTCTATAGA-GC----TTGAGAGCCTTCAGCCTCCCGACACATTCCT-TGG
|||||
TGCTCTCCCTACCTTTCAATATAGTAGACAACTTAAGAACCTTGAAAGAGCCAC-TTCCTCTGG
750 760 770 780 790 800 810
860 870 880 890 900 910
ATTACAGCTGTACTTCCAA---CAGTTATATATATGTGTGATGTTTCTGTCTATATCTATGAAATGGAAG
|||||
ATTCCGGCTGTACTTGTATATGTTGTGTTTGTGGAGTGTGCTTTTAAACAATAAGAAA---AGG
820 830 840 850 860 870 880
920 930 940 950 960 970 980 990
AAGAAAGAGCGGCTTCGCAACTCTTATTAATGTGGAAACCAACAAATGAGAGGGAAGAGTGAACAGACC
|||||
AAGAAAGAGCAGCCTGGGCCCCCTCTCATGATGTGAACCATCAAAAGGAGAGAAAAGAGCAACAGACC
890 900 910 920 930 940 950
1000 1010 1020 1030 1040 1050 1060
AAGAAAGAGAAAAAATCCATATACTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTGAAAGACA
|||||
AACGAAAGAGTACCATACCAAGTACTGTAGAGATCTGATGAAGCCAGGTGTG--TTAACATTTTGAAGACA
960 970 980 990 1000 1010 1020
1070 1080 1090 1100 1110 X
TCTTCATGCGACAAAGTGA-TA--CATGTTTTTAATTAAAGTAAAGTAAAGCCCAAAAAAAA
|||||
GCCTCAAGGGGCAAAAAATCAGTAGAAGAAATGTGGCTT--GACGT--GCTGACAT
1030 1040 1050 1060 1070 1080
```

> O < IntellGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
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Results file 5942607-2_x_303510-6.res made by epaula on Tue 17 Aug 104 16:36:51-EST.

Query sequence being compared: US-08-101-624-2 (1-329)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-08-101-624-2 (1-329) with:
File : US09303510Amod.pep

100-
N -
U 50-
M -
B -
R -
R -
O -
F 10-
S -
S 5-
O -
U -
E -
N -
C -
B -
S 0
-SCORE 0 13 25 38 51 63 76 89 101 114
STDV

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2
Mismatch penalty 1.00 Joining penalty 20
Gap penalty 0.05 Window size 329
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 114 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00
Number of residues: 329
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. US-08-101-624-2 (1-329)	US-09-303-510-6 Sequence 6, Application US 09303510A	329	114	0.00
Initial Score = 114 Optimized Score = 184 Significance = 0.00				
Residue Identity = 57% Matches = 192 Mismatches = 130				
Gaps = 10 Conservative Substitutions = 0				
X	MDPQCTMGISNIIIFVMAFLSGAAPLKIQAIFNETADLPQCFANSONOSLSSELYVFWQDQENLVLANEYVIG	10	20	30
X	MGICDSTWGLSHTLLVMAFLSGVSSMKSQAYFNTGELPCHFTNSONISLDELVFWQDQKLVLYEIRFG	10	20	30
X	KEKPSVSHSKYMGRTSPDSWTLRLNLIQIKDKGLYOCIIHKKPTGKIRIHONKSELSTLANFSQPEIVP	80	90	100
X	KENPQVHLKYGKRTSPDKDNTLRLNLIQIKDKGLYOCIIHKKPTGKIRIHONKSELSTLANFSQPEITV	80	90	100
X	ISNITBN-VYINLTGSSIHGYPPEPKMSVLTFTKNSITLEYDGIQKSDQNTVELYDVISLSVSFPDVTSM	150	160	170
X	TSNRTENSGIIMLTGSSIOGYPEPKEMFOLNTENSTTKYDVMKKSQNNVTLEYVNSISLPSVP-EAHNV	150	160	170
X	TIFC--ILETDKTRLLSSPFI--ELEDPQPPDHI PWITAVL-PTVYIICVAVFCLIIKKMKKKRPRNSYK	220	230	240
X	SVFCALKLET-LEMILSLPFINIDAPKDKDPEQGHFLMAVLVAFVFCGAVSFKTLRK-RKKQOPGSHH	220	230	240
X	CCTNTERESESQTKREKIHIPERSDEAQRVFKSKTSKCDPTCF	290	300	310
X	CETIKRERKESKQTERVYPVHVPERSDEACV-NILKTPASGDKNQ	290	300	310